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OM protein - protein search, using sw model

Run on: February 2, 2005, 18:26:32 ; Search time 151 Seconds
(without alignments)
28.508 Million cell updates/sec

Title: US-10-634-645-1

Perfect score: 54

Sequence: 1 AAVLLPVLAAAP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	12	2 AAY44160	Membrane-
2	54	100.0	12	4 AAE02980	Hydrophob
3	54	100.0	12	4 AAU00644	Human mem
4	54	100.0	12	5 ABG78983	Cell pene
5	54	100.0	12	5 AAU78350	Grb2 SH2
6	54	100.0	12	5 ABB81929	Cystic fi
7	54	100.0	12	5 ABG75508	Signal-se
8	54	100.0	12	5 ABB81178	Grb2 SH2
9	54	100.0	12	5 AAU77231	Synthetic
10	54	100.0	12	6 AAE32085	Transport
11	54	100.0	12	7 ADB88787	Membrane
12	54	100.0	12	7 ADC22455	Protein-d
13	54	100.0	12	7 ADG28018	Kaposi FG
14	54	100.0	12	7 ADH76185	Transduct
15	54	100.0	12	7 ADL88654	MPS (Kapo
16	54	100.0	12	7 ADM60178	Novel rec
17	54	100.0	12	8 ADG12916	Cytoplasm
18	54	100.0	12	8 ABG75425	Kaposi's
19	54	100.0	12	8 ABG75438	Membrane
20	54	100.0	12	8 ADJ78876	Src homol
21	54	100.0	12	8 ADL14687	Cardiant
22	54	100.0	12	8 ADK15575	Membrane
23	54	100.0	12	8 ADO26467	Grb2 SH2
24	54	100.0	13	5 ABG68407	Membrane
25	54	100.0	14	8 ABG75427	Membrane

ALIGNMENTS

RESULT 1

AA44160

ID AAY44160 standard; protein; 12 AA.

XX AC AAY44160;

XX AC

DT 01-FEB-2000 (first entry)

XX DE Membrane-translocating peptide sequence.

XX KW Membrane-translocating peptide sequence; MTS; fusion protein; production;

KW Schistosoma japonicum; glutathione S transferase; adenovirus; mammal;

KW p53; immune response; hepatitis B virus; surface antigen; canine; feline;

KW protease inhibitor; cancer; tumor suppressor; bovine.

XX OS Synthetic.

XX PN WO9949879-A1.

XX PD 07-OCT-1999.

XX PF 31-MAR-1999; 99WO-US007189.

XX PR 31-MAR-1998; 98US-0080083P.

XX PR 04-NOV-1998; 98US-00186170.

XX PA (UYVA-) UNIV VANDERBILT.

XX PI Lin Y, Donahue JP, Rojas M, Tan ZJ;

XX DR WPI; 1999-610819/52.

XX DR N-PSDB; AA228749.

XX PT New peptides containing a membrane-translocating sequence used to develop

XX PT products for use in, e.g. vaccines.

XX PS Claim 1; Page 66; 85pp; English.

XX CC This sequence represents a novel membrane-translocating peptide sequence

XX CC (MTS). The invention relates to the use of the MTS peptides for

XX CC generating fusion proteins which can be used for the production of

XX CC polypeptides of interest such as Schistosoma japonicum glutathione S

XX CC transferase, an adenovirus E3 19K protein or a mammalian p53 protein.

XX CC Fusions of the peptides can also be used for inducing an immune response

XX CC in a mammal using e.g. a viral polypeptide such as hepatitis B surface

XX CC antigen. They can also be used for protecting a subject from an

XX CC infectious agent using a polypeptide that inhibits reproduction of the

XX CC infectious agent such as a protease inhibitor. They can also be used for

Abp70234 Amino aci
Abp70214 Amino aci
Abp70217 Amino aci
Abg75426 Membrane
Aau00633 Human mem
Aau00635 Human mem
Abp70215 Amino aci
Adb88778 Membrane
Adb88776 Membrane
Abg75429 Membrane
Aay44170 Fragment
Aau00655 Human tar
Aau00634 Human mem
Adb88777 Membrane
Abg75428 Membrane
Abg79150 Cell pene
Abp70216 Amino aci
Aau00632 Human mem
Abg79149 Cell pene
Adb88775 Membrane

54 100.0 15 6 ABP70234
54 100.0 15 6 ABP70214
54 100.0 15 6 ABP70217
54 100.0 15 8 ABG75426
54 100.0 16 4 AAU00633
54 100.0 16 4 AAU00635
54 100.0 16 6 ABP70215
54 100.0 16 7 ADB88778
54 100.0 16 7 ADB88776
54 100.0 16 8 ABG75429
54 100.0 19 2 AAY44170
54 100.0 19 4 AAU00655
54 100.0 19 4 AAU00634
54 100.0 19 7 ADB88777
54 100.0 19 8 ABG75428
54 100.0 20 5 ABG79150
54 100.0 20 6 ABP70216
54 100.0 21 4 AAU00632
54 100.0 21 5 ABG79149
54 100.0 21 7 ADB88775

CC treating cancer using a polypeptide tumor suppressor such as p53 protein
 CC or a polypeptide inhibitor of Bcl-2. The methods can be used for treating
 CC canine, feline and bovine diseases and also for studying intracellular
 CC proteins
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
 |||||
 Db 1 AAVLLPVLLAAP 12

RESULT 2
 AAE02980
 ID AAE02980 standard; peptide; 12 AA.

XX AC AAE02980;
 XX 10-AUG-2001 (first entry)
 XX Hydrophobic protein transduction domain #8.

XX Peptide monomer; nuclear localisation sequence; NLS;
 XX protein transduction domain; PTD; molecule transfer.

XX Unidentified.

XX WO200138547-A2.

XX 31-MAY-2001.

XX 23-NOV-2000; 2000WO-EP011690.

XX 24-NOV-1999; 99EP-00123423.

XX (ROSE/) ROSENECKER J.

XX (RITT/) RITTER W.

XX (RUDO/) RUDOLPH C M.

XX (PLAN/) PLANK C.

XX Rosenacker J, Ritter W, Rudolph CM, Plank C;

XX WPI; 2001-367696/38.

XX Novel polypeptides comprising at least two monomers which comprise a
 XX nuclear localization sequence and protein transduction domain,
 XX respectively useful for transferring nucleic acid molecules into
 XX eukaryotic cells.

XX Claim 3; Page 32; 68pp; English.

XX The present invention relates to a polypeptide comprising at least two
 XX peptide monomers, in which each peptide monomer comprises an amino acid
 XX sequence which serves as a nuclear localisation sequence (NLS) or an
 XX amino acid sequence which serves as protein transduction domain (PTD) in
 XX eukaryotic cells. The polypeptide of the invention is used for
 XX transferring a molecule into eukaryotic cells. The use of a polypeptide
 XX comprising NLS or PTD drastically increases the efficiency of the
 XX transfer of attached molecules, preferably negatively charged molecules
 XX into the nucleus or cytoplasm of a eukaryotic cell. The present sequence
 XX is hydrophobic PTD which include the sequence of transportan

XX Sequence 12 AA;

Query Match 100.0%; Score 54; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12

Db 1 AAVLLPVLLAAP 12
 |||||

RESULT 3
 AAU00644
 ID AAU00644 standard; peptide; 12 AA.

XX AAU00644;

XX 07-SEP-2001 (first entry)

XX Human membrane translocating peptide (MTLP) #13.

XX Membrane translocating peptide; MTLP; human; intracellular gene delivery;
 XX epithelial cell layer; gastrointestinal tract; circulatory system.

XX Homo sapiens.

XX WO200127154-A2.

XX 19-APR-2001.

XX 27-SEP-2000; 2000WO-IB001491.

XX 27-SEP-1999; 99US-0156246P.

XX (OMAH/) O'MAHONY D J.

XX (LAMB/) LAMKIN I J.

XX O'mahony DJ, Lambkin IJ;

XX WPI; 2001-300212/31.

XX N-PSDB; AAS00638.

XX Compositions for enhancing uptake of e.g. drugs or DNA across a cell
 XX membrane, comprise membrane translocating peptides having specific amino
 XX acid sequences or a derivative, fragment, motif, analog or peptidomimetic
 XX of the peptides.

XX Claim 2; Page 11; 42pp; English.

XX The sequence represents a human membrane translocated peptide (MTLP).
 XX MTLPs and their related fragments, motifs, derivatives and analogues are
 XX used for enhancing uptake of a pharmaceutically active agent into a cell,
 XX into or out of an intracellular compartment and across a cell layer (for
 XX example, an epithelial cell layer lining the gastrointestinal tract),
 XX either directly or from a pharmaceutically active agent loaded particle,
 XX into the circulatory system of an animal. This method is useful for
 XX intracellular gene delivery, as a rapid screening method for the
 XX identification of MTLPs which retain the functional activity of a full-
 XX length MTLP, as a cell-based screen for assaying the functional activity
 XX of a MTLP and characterising the properties of a MTLP, for diagnosis of a
 XX pathological disorder (by administration of a MTLP-active agent complex
 XX or MTLP-active particle complex comprising a diagnostic agent) and for
 XX preventing or treating a pathological disorder

XX Sequence 12 AA;

Query Match 100.0%; Score 54; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
 |||||

Db 1 AAVLLPVLLAAP 12

RESULT 4
 ABG78983
 ID ABG78983 standard; peptide; 12 AA.

XX ABG78983;

XX	DT	15-NOV-2002 (first entry)
XX	DE	Cell penetrating peptide CPP1.
XX	KW	Cell penetrating peptide; cancer; tumour; melanoma; thymoma; lymphoma;
XX	KW	sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
XX	KW	Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
XX	KW	kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
XX	KW	ovarian cancer; pancreatic cancer; vaccine; dendritic cell;
XX	KW	tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
XX	KW	cytostatic.
XX	OS	Unidentified.
XX	PN	WO200264057-A2.
XX	PD	22-AUG-2002.
XX	Pf	15-FEB-2002; 2002WO-US005212.
XX	PR	15-FEB-2001; 2001US-0268687P.
-XX	PA	(BAYU) BAYLOR COLLEGE MEDICINE.
XX	PI	Wang R;
XX	DR	WPI; 2002-627577/67.
XX	PT	Novel composition for treating a disease in an animal, comprises an
XX	PT	immune effector cell and cell penetrating peptide associated with an
XX	PT	antigen or antibody.
XX	PS	Disclosure; Page 10; 61pp; English.
XX	CC	The invention relates to a composition (I) comprising an immune effector
XX	CC	cell and a cell penetrating peptide (CPP) associated with an antigen or
XX	CC	antibody. Also included are (1) a vaccine comprising (I), CPP associated
XX	CC	with an antigen, and a pharmaceutically acceptable carrier and (2)
XX	CC	preparing a composition for a disease, by providing (I) and CPP
XX	CC	associated with an antigen for disease, and introducing the antigen-
XX	CC	associated CPP to (I), where antigen enters into the cell. The antigens
XX	CC	are, for example, tumour antigen derived epitopes recognised by tumour
XX	CC	infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
XX	CC	or II. The composition is useful for enhancing immunity in an animal to a
XX	CC	disease, by administering a mature dendritic cell comprising CPP
XX	CC	associated with an antigen to disease, to the animal, such that following
XX	CC	the administration, animal is protected from disease, where the animal
XX	CC	comprises both CD4+ and CD8+ T cells. It is also useful for treating a
XX	CC	disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
XX	CC	cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
XX	CC	cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
XX	CC	breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
XX	CC	The animal is further subjected to a cancer treatment including surgery,
XX	CC	radiation, chemotherapy or gene therapy. The administration of (I),
XX	GC	preferably dendritic cell is prior to, subsequent to or concurrent with,
XX	CC	the cancer treatment. The present sequence is cell penetrating peptide of
XX	SQ	Sequence 12 AA;
		Query Match 100.0%; Score 54; DB 5; Length 12;
		Best Local Similarity 100.0%; Pred. No. 0.0098;
		Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy		1 AAVLLPVLLAAP 12
Dd		1 AAVLLPVLLAAP 12
RESULT 5		
ID		AAU78350 standard; peptide; 12 AA.

XX	DT	18-JUN-2002 (first entry)
XX	DE	Grb2 SH2 domain derived signal peptide.
XX	KW	Membrane translocation signal; signal sequence based peptide I;
XX	KW	red blood cell vehicle; polypeptide delivery; Grb2; SH2 domain.
XX	OS	Unidentified.
XX	PN	WO200207752-A2.
XX	PD	31-JAN-2002.
XX	Pf	24-JUL-2001; 2001WO-GB003327.
XX	PR	24-JUL-2000; 2000WO-GB002848.
PR	PR	09-AUG-2000; 2000WO-GB003056.
PR	PR	01-FEB-2001; 2001WO-GB000417.
PR	PR	16-FEB-2001; 2001US-00785802.
XX	PA	(GEND-) GENDEL LTD.
XX	PI	Craig R;
XX	DR	WPI; 2002-280593/32.
XX	PT	Preparing a red blood cell vehicle suitable for delivering an agent to a
XX	PT	target site in a vertebrate due to loading the red blood cell with an
XX	PT	agent-membrane translocation sequence.
XX	PS	Disclosure; Page 45; 135pp; English.
XX	CC	The invention describes a method of preparing a red blood cell vehicle
XX	CC	suitable for delivering an agent to a target site in a vertebrate
XX	CC	comprising providing a red blood cell and loading the red blood cell with
XX	CC	an agent-MTS (membrane translocation sequence) conjugate. The red blood
XX	CC	cells produced may be used in the preparation of a medicament for
XX	CC	delivery of an agent to or at a target site and of one or more agents to
XX	CC	a vertebrate. The agent is actively released from the red blood cell
XX	CC	vehicle by application of a stimulus to disrupt the red blood cell
XX	CC	vehicle. This sequence represents signal sequence derived from the Grb2
XX	CC	SH2 domain, one of the membrane translocation peptides tested in the
XX	SQ	Sequence 12 AA;
		Query Match 100.0%; Score 54; DB 5; Length 12;
		Best Local Similarity 100.0%; Pred. No. 0.0098;
		Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy		1 AAVLLPVLLAAP 12
Dd		1 AAVLLPVLLAAP 12
RESULT 6		
ID		ABB81929 standard; peptide; 12 AA.
XX	AC	ABB81929;
XX	DT	30-OCT-2002 (first entry)
XX	DE	Cystic fibrosis fusion protein membrane translocation sequence.
XX	DE	Cystic fibrosis; transmembrane conductance regulator; CFTR; membrane;
XX	KW	translocation sequence; MTS; gastrointestinal; respiratory; hepatotropic.
XX	OS	Synthetic.

XX DR WPI; 2002-280593/32.

XX PT Preparing a red blood cell vehicle suitable for delivering an agent to a

XX PT target site in a vertebrate due to loading the red blood cell with an

XX PT agent-membrane translocation sequence.

XX PS Disclosure; Page 9; 43pp; English.

XX CC The invention discloses a method for preparing a delivery vehicle for

XX CC delivering an agent to a target site in a vertebrate. The method

XX CC comprises loading a cell with an agent-membrane translocation sequence

XX CC (MTS) conjugate, which contains a membrane translocation sequence

XX CC enabling the agent to cross the plasma membrane of a cell. Also disclosed

XX CC is a pharmaceutical composition comprising a red blood cell for delivery

XX CC of an agent to a vertebrate, the red blood cell comprising the novel

XX CC agent-MTS conjugate and a method of immunization of an animal with an

XX CC antigen. The method is useful for preparing delivery vehicles,

XX CC particularly a red blood cell, for the intracellular delivery of a

XX CC therapeutic agent to a target site. The method is particularly useful for

XX CC enabling an agent to cross the plasma membrane of a target cell, and for

XX CC selectively releasing the agent-MTS conjugate at a target site to

XX CC facilitate the uptake of the agent by the cells at the target site. The

XX CC preferred MTS sequences are from HIV-1 trans-activating protein (Tat),

XX CC Drosophila Antennapedia homeodomain protein (Antp-HD), Herpes Simplex-1

XX CC virus VP22 protein (HSV-VP22), a signal-sequence-based peptide and a

XX CC Transportan and Amphiphilic model peptide. The sequence presented is the

XX CC Signal-sequence-based peptide III, which is derived from the Grb2 SH2

XX CC (not defined) domain

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 5; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0098;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12

DB 1 AAVLLPVLLAAP 12

RESULT 8

ABB81178

ID ABB81178 standard; peptide; 12 AA.

AC ABB81178;

XX DT 25-NOV-2002 (first entry)

XX DE Grb2 SH2 domain derived peptide fragment.

XX KW Red blood cell; RBC; virus; vertebrate; therapeutic; tissue imaging;

XX KW Grb2; SH2 domain; membrane translocation.

XX OS Unidentified.

XX FN WO200260416-A1.

XX PD 08-AUG-2002.

XX PF 01-FEB-2002; 2002WO-GB000437.

XX PR 01-FEB-2001; 2001GB-00002561.

XX PR 16-FEB-2001; 2001US-0269528P.

XX PA (GEND-) GENDEL LTD.

XX PI McHale AP, Craig R;

XX XX WPI; 2002-643355/69.

XX PT Delivering agent to target site in vertebrate comprises loading red blood

XX PT cell with virus or virus-like particle comprising agent, sensitizing

XX PT

PN WO200258627-A2.

XX PD 01-AUG-2002.

XX PF 09-NOV-2001; 2001WO-US049958.

XX PR 09-NOV-2000; 2000US-0247494P.

XX PA (UYVA-) UNIV VANDERBILT.

XX PI Stecenko A, Brigham K;

XX XX WPI; 2002-590789/63.

XX PT Fusion protein, useful in the treatment of cystic fibrosis or

XX PT dysfunctions of the gastrointestinal tract or liver, comprises cystic

XX PT fibrosis transmembrane conductance regulator and a membrane translocation

XX PT sequence.

XX PS Claim 3; Page 15; 19pp; English.

XX CC The invention relates to a novel fusion protein comprising a cystic

XX CC fibrosis transmembrane conductance regulator (CFTR) and a membrane

XX CC translocation sequence (MTS). The sequence represents the membrane

XX CC translocation sequence. The fusion protein of the invention has

XX CC gastrointestinal, respiratory, and hepatotropic activity. The protein is

XX CC taken up by affected cells and thereby used for treating cystic fibrosis

XX CC or dysfunctions of the gastrointestinal tract or liver

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 5; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0098;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12

DB 1 AAVLLPVLLAAP 12

RESULT 7

ABG75508

ID ABG75508 standard; peptide; 12 AA.

AC ABG75508;

XX DT 14-APR-2003 (first entry)

XX DE Signal-sequence-based peptide III.

XX KW Translocation; delivery vehicle; agent-membrane translocation sequence;

XX KW MTS; membrane translocation sequence; plasma membrane; red blood cell;

XX KW immunisation; antigen; intracellular delivery; therapeutic; HIV-1;

XX KW trans-activating protein; Tat; Antennapedia homeodomain protein; Antp-HD;

XX KW VP22 protein; HSV-VP22; signal-sequence-based peptide; Transportan;

XX KW Amphiphilic model peptide; Grb2 SH2.

XX OS Unidentified.

XX PN US2002151004-A1.

XX PD 17-OCT-2002.

XX PF 16-FEB-2001; 2001US-00785802.

XX PR 24-JUL-2000; 2000WO-GB002848.

XX PR 09-AUG-2000; 2000WO-GB003056.

XX PR 22-DEC-2000; 2000US-00748063.

XX PR 22-DEC-2000; 2000US-00748789.

XX PA (CRAI/) CRAIG R.

XX XX Craig R;

XX PI

PT cell, introducing cell into vertebrate and applying energy to release
PT virus particle from cell.
PS Disclosure; Page 55; 87pp; English.
XX
CC The invention relates to delivering an agent to a target site in a
CC vertebrate. The method involves (a) loading a red blood cell (RBC) with a
CC virus or a virus-like particle (VLP) comprising an agent; (b) sensitizing
CC RBC to render it more susceptible to disruption than unsensitized RBC;
CC (c) introducing RBC into a vertebrate, and (d) applying energy to release
CC (i). Steps (a) and (b) may be performed in any order. (ii) (RBC loaded
CC with a virus or a virus-like particle comprising a therapeutic agent) is
CC useful for the delivery of a therapeutic agent to a target site in a
CC vertebrate, or in the preparation of a medicament for delivery of a
CC therapeutic agent to a target site in a vertebrate. (ii) is also useful
CC for delivering one or more agents to a vertebrate and for treating or
CC preventing a disease. The method is useful for delivering agents such as
CC those useful for imaging of tissues in vivo or ex vivo, preferably for
CC delivering an agent to a subcellular organelle such as nucleus,
CC mitochondria, Golgi or endoplasmic reticulum. The present sequence
CC represents a Grb2 SH2 domain derived peptide fragment, used for membrane
CC translocation
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVLLPVLAAAP 12
DB 1 AAVLLPVLAAAP 12
|||||
RESULT 9
AAU77231
ID AAU77231 standard; peptide; 12 AA.
XX
AC AAU77231;
XX
DT 05-JUN-2002 (first entry)
XX
DE Synthetic pcDNA3-E7/MTS peptide sequence.
XX
KW Virucide; cytostatic; vaccine; intercellular transport; antigenic;
KW immune response; cytotoxic T lymphocyte; tumour; cancer; pcDNA3-E7/MTS;
KW chronic viral infection; veterinary herpesvirus infection; pseudorabies;
KW equine herpesvirus; bovine herpesvirus; Marek's disease virus; chicken;
KW fowl; animal retroviral disease; rabies.
XX
OS Synthetic.
XX
XX WO200209645-A2.
XX
XX 07-FEB-2002.
XX
XX 01-AUG-2001; 2001WO-US023966.
XX
XX 01-AUG-2000; 2000US-0222185P.
XX
XX 15-FEB-2001; 2001US-0268575P.
XX
XX 04-APR-2001; 2001US-0281004P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Wu T, Hung C;
XX
XX WPI; 2002-257367/30.
XX
XX N-PSDB; ABK11804.
XX
XX New nucleic acids encoding fusion polypeptide comprising intercellular
XX transport polypeptide linked to antigenic polypeptide, useful as
XX therapeutic vaccine for cancer and major chronic viral infections.
XX

PS Example 1; Page 39; 102pp; English.
XX
CC The present invention relates to a new nucleic acid molecule that encodes
CC a fusion polypeptide. The fusion protein comprises a first polypeptide
CC comprising at least one intercellular transport polypeptide and a second
CC polypeptide comprising at least one antigenic polypeptide or peptide. The
CC invention also describes an optional linker peptide linking the first and
CC second polypeptide. The nucleic acid is useful as a vaccine for enhancing
CC immune responses, primarily cytotoxic T lymphocyte responses to specific
CC antigens such as tumour or viral antigens. The compositions comprising
CC the nucleic acids are especially useful as a therapeutic vaccine for
CC cancer and for major chronic viral infections, as well as in the
CC treatment of veterinary herpesvirus infections, including equine or
CC bovine herpesvirus, Marek's disease virus in chickens and other fowl,
CC animal retroviral diseases, pseudorabies and rabies. The present amino
CC acid sequence represents the peptide used in the methods of the invention
CC for the generation of pcDNA3-E7/MTS expression vector
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVLLPVLAAAP 12
DB 1 AAVLLPVLAAAP 12
|||||
RESULT 10
AAE32065
ID AAE32065 standard; peptide; 12 AA.
XX
AC AAE32065;
XX
DT 24-MAR-2003 (first entry)
XX
DE Transport peptide used in the invention.
XX
KW Drug delivery construct; axon growth; nerve injury; ischaemic damage;
KW stroke injury; gene therapy; neuroleptic; neuroprotective.
XX
OS Unidentified.
XX
XX WO200283179-A2.
XX
XX 24-OCT-2002.
XX
XX 08-APR-2002; 2002WO-CA000480.
XX
XX 12-APR-2001; 2001CA-02342970.
XX
XX 13-NOV-2001; 2001CA-02362004.
XX
XX 15-JAN-2002; 2002CA-02367636.
XX
XX (BIOA-) BIOAXONE THERAPEUTIQUE INC.
XX
XX McKerracher L;
XX
XX WPI; 2003-092963/08.
XX
XX New drug delivery construct comprising a transport and active agent
XX region, useful for the manufacture of a pharmaceutical composition for
XX treating nerve injury.
XX
XX Disclosure; Page 52; 189pp; English.
XX
XX The invention relates to a new drug delivery construct comprising at least
XX one transport agent region and an active agent region. The transport
XX agent region is able to facilitate the uptake of the active agent region
XX into a cell. The active agent region is an active therapeutic agent
XX region able to facilitate axon growth and an analogue. The drug delivery
XX construct is useful for suppressing the inhibition of neuronal axon
XX growth, facilitating axon growth, treating nerve injury, treating

CC ischaemic damage related to stroke injury. The drug delivery construct
CC and the drug conjugate are useful for the manufacture of a pharmaceutical
CC composition for treating nerve injury. The invention is useful in gene
CC therapy. The present sequence is transport peptide used in the invention
XX
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVLLPVLLAAP 12
DB 1 AAVLLPVLLAAP 12
RESULT 11
ID ADB88787 standard; peptide; 12 AA.
XX
XX ADB88787;
XX 04-DEC-2003 (first entry)
XX Membrane translocating peptide #13.
XX Peyer's patch cell; non-Peyer's patch cell; transcription factor;
XX upregulated protein; antigen; vaccine delivery; M cell;
XX membrane translocating peptide.
XX Unidentified.
XX WO2003004646-A2.
XX 16-JAN-2003.
XX 04-APR-2002; '2002MO-IB003866.
XX 02-APR-2001; 2001US-0281387P.
XX 04-JUL-2001; 2001US-0302591P.
XX (OMAH/) O'MAHONY D J.
XX O'mahony DJ, Byrne D, Brayden D;
XX WPI; 2003-229409/22.
XX Increasing the levels of a protein in a Peyer's patch cell, useful for
XX targeted vaccine or drug delivery, comprises delivering to the Peyer's
XX patch cell a transcription factor or an activator of a transcription
XX factor.
XX Example 6; Page 51; 147pp; English.
XX The invention relates to a novel method for increasing the levels of a
XX protein in a Peyer's patch cell. The method comprises delivering to the
XX cell a nucleic acid coding for a protein, the level of which or its mRNA
XX is greater than in a non-Peyer's patch cell. The preferred protein of the
XX invention is a transcription factor or a protein that activates a
XX transcription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3
XX -signal transducer and activator of transcription 3, Nfkapabgr; Tf p105
XX subunit, S-myc proto-oncogene, myc related, Nm23-M2, nucleoside
XX diphosphate kinase B, metataseis reducing protein, and C-est-J proto-
XX onogene, and p54. The preferred upregulated protein of the invention is
XX selected from clusterin, T-cell surface glycoprotein CD5 precursor, Hsp
XX 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a
XX protein selected from the group. The method is useful for increasing or
XX decreasing the level of a protein in a Peyer's patch cell, particularly
XX in increasing antigen or vaccine delivery to M cells. The method may also
XX be used to enhance transport of a drug through the gastrointestinal tract
XX (GIT). This sequence represents a membrane translocating peptide of the
XX invention.
XX

SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVLLPVLLAAP 12
DB 1 AAVLLPVLLAAP 12
RESULT 12
ID ADC22455 standard; peptide; 12 AA.
XX
XX ADC22455;
XX 18-DEC-2003 (first entry)
XX Protein-derived transport peptide SEQ ID NO:304.
XX recombinant fusion protein; fusion protein; binding; detection;
XX localisation domain; binding domain;
XX subcellular compartment localisation.
XX Synthetic.
XX WO2003012068-A2.
XX 13-FEB-2003.
XX 01-AUG-2002; 2002WO-US024572.
XX 01-AUG-2001; 2001US-0309395P.
XX 13-DEC-2001; 2001US-0341589P.
XX (CELL-) CELLOMICS INC.
XX Bright G, Premkumar DR, Chen Y;
XX WPI; 2003-248174/24.
XX New recombinant fusion protein comprising detection and first
XX localization domains and a binding domain for the molecule of interest,
XX useful for detecting binding of a molecule of interest.
XX Disclosure; SEQ ID NO 304; 101pp; English.
XX The present invention describes a recombinant fusion protein (I) for
XX detecting binding of a molecule of interest. (I) comprises: (a) a
XX detection domain; (b) a first localisation domain; and (c) a binding
XX domain for the molecule of interest. The detection domain, the first
XX localisation domain and the binding domain for the molecule of interest
XX constituting the recombinant fusion protein for detecting binding of a
XX molecule of interest are operably linked. The binding domain for the
XX molecule of interest is separated from the first localisation domain by 0
XX -20 amino acid residues. The first localisation domain and the binding
XX domain for the molecule of interest both do not occur in a single non-
XX recombinant protein with the same spacing as in the recombinant fusion
XX protein for detecting binding of a molecule of interest. Also described:
XX (1) a recombinant nucleic acid encoding the recombinant fusion protein;
XX (2) a recombinant expression vector comprising the nucleic acid control
XX sequences operably linked to the recombinant nucleic acid molecule; (3) a
XX genetically engineered host cell transfected with the recombinant
XX expression vector; (4) a kit for detecting binding of the molecule of
XX interest; and (5) a method for identifying compounds that alter the
XX binding of the molecule of interest. The recombinant fusion protein is
XX useful for detecting binding of a molecule of interest. The recombinant
XX fusion protein eliminates the need to construct two or more chimeric
XX proteins and enables the monitoring of biochemical events in live, intact
XX or fixed cells. The present sequence is used in the exemplification of
XX the present invention.
XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 AAVLLPVLAAAP 12

RESULT 13
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 AC ADG28018;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Kaposi FGF signal membrane fusion sequence seq id 19.
 KW fusion protein; cold shock domain; membrane translocation sequence; CspA;
 KW CspB; CspC; CspD; rpl S1 binding domain; eukaryotic Y-box protein;
 KW DNA binding protein B; DBPB; DBPA; EFE-1; mRNFP3; mRNFP4; FRG Y1;
 KW nuclease-sensitive element binding protein 1; NSEP 1;
 KW DNA condensation domain; DNA binding domain; SPKR;
 KW nuclear localisation sequence; NLS; protein purification tagged sequence;
 KW gene delivery; kaposi's sarcoma-associated herpesvirus;
 KW FGF signal sequence; membrane fusion sequence.
 XX
 OS Human herpesvirus 8.
 XX
 PN US2003211590-A1.
 XX
 PD 13-NOV-2003.
 XX
 PF 13-MAY-2002; 2002US-00144549.
 XX
 PR 13-MAY-2002; 2002US-00144549.
 XX
 PA (HWUP/) HWU P L.
 XX
 PI Hwu PL;
 DR WPI; 2003-501590/82.
 XX
 PT New fusion protein comprising a cold shock domain, and a membrane
 PT translocation sequence, useful for delivering DNAs and RNAs to in vivo
 PT cells for gene delivery.
 XX
 PS Claim 9; SEQ ID NO 19; 24pp; English.
 XX
 CC The invention describes a fusion protein for delivery of a desired
 CC molecule into cells or nuclei, comprising a cold shock domain, its
 CC homologue and functional derivative, and a membrane translocation
 CC sequence or its functional equivalent peptides and/or derivatives. The
 CC fusion protein comprises a cold shock domain that is selected from CspA,
 CC CspB, CspC, CspD, rpl S1 binding domain, eukaryotic Y-box proteins, DNA
 CC binding protein B (DBPB), DBPA, EFE-1, mRNFP3, mRNFP4, FRG Y1 and nuclease-
 CC sensitive element binding protein 1 (NSEP 1). The functional equivalent
 CC derivative of cold shock protein is modified by inserting into the cold
 CC shock domain with a DNA condensation domain or a DNA binding domain. The
 CC DNA condensation or binding domain is selected from DNA condensation
 CC domain (SPKR) 3-4 and the positive charge nuclear localisation sequences
 CC (NLS+). The membrane transduction sequence is protein transduction domain
 CC (PTD) or membrane fusion sequence. The fusion protein further comprises a
 CC protein purification tagged sequence selected from HA, GST, and His6 tag.
 CC The fusion protein is useful for delivering DNAs and RNAs to in vivo
 CC cells for gene delivery or for delivering nucleic acids to an embryo or
 CC to a living animal for the production of transgenic animal. This is the
 CC amino acid sequence of a membrane fusion sequence derived from Kaposi's
 CC sarcoma-associated herpesvirus FGF signal sequence.

SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 7; Length 12;
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 DB 1 AAVLLPVLAAAP 12

RESULT 14
 ADH76185
 ID ADH76185 standard; peptide; 12 AA.
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 AC ADH76185;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Transduction domain peptide of the invention SEQ ID NO:286.
 KW heat shock protein 20; cytosolic; antiarteriosclerotic; vasotropic;
 KW antianginal; cerebroprotective; antiarrhythmic; antiasthmatic;
 KW gynaecological; hypotensive; antimigraine; tocolytic; relaxant; HSP;
 KW smooth muscle cell; smooth muscle cell; transduction domain.
 XX
 OS Synthetic.
 XX
 PN WO2003018758-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 23-AUG-2002; 2002WO-US026918.
 XX
 PR 23-AUG-2001; 2001US-0314535P.
 XX
 PA (UYAR-) UNIV ARIZONA.
 PA (BROP/) BROPHY C.
 PA (KONA/) KOMALAVILAS P.
 PA (PANI/) PANITCH A.
 PA (SEAL/) SEAL B.
 PA (LOKE/) LOKESH J.
 XX
 PI Brophy C, Komalavilas P, Panitch A, Seal B, Lokesh J;
 DR WPI; 2003-393248/37.
 XX
 PT New heat shock protein 20-derived polypeptides, useful for inhibiting,
 PT treating or preventing smooth muscle cell vasospasm or a disorder such as
 PT intimal hyperplasia, restenosis, atherosclerosis or smooth muscle cell
 PT tumors.
 XX
 PS Claim 29; SEQ ID NO 286; 194pp; English.
 XX
 CC The invention relates to a novel polypeptide comprising a heat shock
 CC protein 20-derived polypeptide. A polypeptide of the invention has
 CC cytosolic, antiarteriosclerotic, vasotropic, antianginal,
 CC cerebroprotective, antiarrhythmic, antiasthmatic, gynaecological,
 CC hypotensive, antimigraine, tocolytic, and relaxant activity, and may act
 CC as a HSP agonist or antagonist. The polypeptides, heat shock protein
 CC (HSP) 20, and methods are useful for treating or preventing a disorder,
 CC e.g. intimal hyperplasia, stenosis, restenosis, transplant vasculopathy,
 CC atherosclerosis, smooth muscle cell tumours such as leiomyosarcoma, or
 CC vasospasm, which is associated with angina, coronary vasospasm,
 CC Prinzmetal's angina, coronary ischaemia, stroke, bradycardia,
 CC hypertension, pulmonary (lung) hypertension, asthma (bronchospasm),
 CC toxemia of pregnancy, pre-term labour, pre-eclampsia/eclampsia, Raynaud's
 CC disease, Raynaud's phenomenon, haemolytic-uremia, non-occlusive
 CC mesenteric ischaemia, anal fissure, achalasia, impotence, migraine, or
 CC ischaemic muscle injury associated with smooth muscle spasm. The
 CC polypeptides and HSP 20 are also useful for inhibiting smooth muscle cell
 CC proliferation and/or migration. The present sequence represents a peptide
 CC used in a polypeptide of the invention.

Fri Feb 4 11:21:31 2005

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XX Sequence 12 AA;
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Query Match 100.0%; Score 54; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 15
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ID ADL88654 standard; peptide; 12 AA.
XX
AC ADL88654;
XX
DT 20-MAY-2004 (first entry)
XX
DE MPS (Kaposi FGF signal sequence) membrane fusion sequence peptide 2.
XX
KW fusion protein; cold shock domain; membrane translocation; gene therapy;
XX transgenic; membrane fusion; MPS; Kaposi FGF signal.
XX
OS Unidentified.
XX
PN JP2004035409-A.
XX
PD 05-FEB-2004.
XX
PF 15-MAY-2002; 2002JP-00140441.
XX
PR 13-MAY-2002; 2002US-00144549.
XX
PA (GENE-) GENESHUTTLE BIOPHARM INC.
XX
PI Hwu PL;
XX
DR WPI; 2003-901590/82.
XX
PT New fusion protein comprising a cold shock domain, and a membrane
PT translocation sequence, useful for delivering DNAs and RNAs to in vivo
PT cells for gene delivery.
XX
PS Claim 9; SEQ ID NO 17; 53pp; Japanese.
XX
CC The invention relates to a novel fusion protein for delivery of a desired
CC molecule into cells or nuclei comprising a cold shock domain, its
CC homologue and functional derivative and a membrane translocation sequence
CC or its functionally equivalent peptides and/or derivatives. The fusion
CC protein of the invention may be useful for delivering DNAs and RNAs to in
CC vivo cells for gene therapy or for delivering nucleic acids to an embryo
CC or to a living animal for the production of transgenic animals. The
CC current sequence is that of a membrane fusion sequence peptide of the
CC invention.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 54; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

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Search completed: February 2, 2005, 18:40:47
Job time : 153 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2005, 18:44:19 ; Search time 144 Seconds
(without alignments)
30.107 Million cell updates/sec

Title: US-10-634-645-1

Perfect score: 54

Sequence: 1 AAVLLPVLLAAP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	100.0	12	9	US-09-789-836-12	Sequence 12, Appl
2	54	100.0	12	9	US-09-785-802A-10	Sequence 10, Appl
3	54	100.0	12	10	US-09-997-455B-4	Sequence 4, Appl
4	54	100.0	12	13	US-10-116-288-1	Sequence 1, Appl
5	54	100.0	12	14	US-10-226-956-286	Sequence 286, App
6	54	100.0	12	14	US-10-077-555-1	Sequence 1, Appl
7	54	100.0	12	14	US-10-211-088-304	Sequence 304, App
8	54	100.0	12	14	US-10-156-570A-27	Sequence 27, Appl
9	54	100.0	12	14	US-10-126-845-1	Sequence 1, Appl
10	54	100.0	12	14	US-10-126-845-14	Sequence 14, Appl
11	54	100.0	12	14	US-10-126-845-72	Sequence 72, Appl
12	54	100.0	12	14	US-10-136-187-1	Sequence 1, Appl
13	54	100.0	12	14	US-10-116-275-102	Sequence 102, App

14	54	100.0	12	14	US-10-144-549-19	Sequence 19, Appl
15	54	100.0	12	15	US-10-361-208-473	Sequence 473, App
16	54	100.0	12	15	US-10-212-410-2	Sequence 2, Appl
17	54	100.0	12	15	US-10-416-285-1	Sequence 1, Appl
18	54	100.0	12	16	US-10-764-235-1	Sequence 1, Appl
19	54	100.0	12	16	US-10-764-235-14	Sequence 14, Appl
20	54	100.0	12	16	US-10-751-380-8	Sequence 8, Appl
21	54	100.0	13	14	US-10-013-815-20	Sequence 20, Appl
22	54	100.0	15	14	US-10-136-845-2	Sequence 2, Appl
23	54	100.0	15	14	US-10-126-845-3	Sequence 3, Appl
24	54	100.0	15	14	US-10-126-845-50	Sequence 60, Appl
25	54	100.0	15	14	US-10-136-845-61	Sequence 61, Appl
26	54	100.0	15	14	US-10-136-187-2	Sequence 2, Appl
27	54	100.0	15	14	US-10-136-187-4	Sequence 4, Appl
28	54	100.0	15	14	US-10-136-187-6	Sequence 6, Appl
29	54	100.0	15	14	US-10-136-187-8	Sequence 8, Appl
30	54	100.0	15	14	US-10-136-187-12	Sequence 12, Appl
31	54	100.0	15	14	US-10-136-187-13	Sequence 13, Appl
32	54	100.0	15	14	US-10-136-187-29	Sequence 29, Appl
33	54	100.0	15	14	US-10-136-187-33	Sequence 33, Appl
34	54	100.0	15	14	US-10-136-187-34	Sequence 34, Appl
35	54	100.0	15	14	US-10-136-187-35	Sequence 35, Appl
36	54	100.0	15	14	US-10-136-187-36	Sequence 36, Appl
37	54	100.0	15	14	US-10-136-187-37	Sequence 37, Appl
38	54	100.0	15	14	US-10-136-187-38	Sequence 38, Appl
39	54	100.0	15	14	US-10-136-187-39	Sequence 39, Appl
40	54	100.0	15	16	US-10-764-235-2	Sequence 2, Appl
41	54	100.0	16	14	US-10-126-845-5	Sequence 5, Appl
42	54	100.0	16	14	US-10-126-845-48	Sequence 48, Appl
43	54	100.0	16	14	US-10-126-845-63	Sequence 63, Appl
44	54	100.0	16	14	US-10-136-187-3	Sequence 3, Appl
45	54	100.0	16	14	US-10-136-187-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-789-836-12
; Sequence 12, Application US/09789836
; Patent No. US20020082204A1
; GENERAL INFORMATION:
; APPLICANT: BRIGHAM, KENNETH L.
; APPLICANT: STECENKO, ARLENE A.
; APPLICANT: SEALY, LINDA
; TITLE OF INVENTION: TREATMENT OF INFLAMMATION WITH P20
; FILE REFERENCE: N-6977
; CURRENT APPLICATION NUMBER: US/09/789,836
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/183,584
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-789-836-12

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Best Local Similarity 100.0%; Pred. No. 0.03; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0

Qy 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 2
US-09-785-802A-10
; Sequence 10, Application US/09785802A

Fri Feb 4 11:21:31 2005

us-10-634-645-1.rapb

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; Patent No. US20020151004A1
; GENERAL INFORMATION:
; APPLICANT: Craig, Roger
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
; FILE REFERENCE: 11067/2035
; CURRENT APPLICATION NUMBER: US/09/785,802A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/748,06
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/748,789
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-802A-10

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAVLLPVLLAAP 12

RESULT 3
US-09-997-465B-4
; Sequence 4, Application US/09997465B
; Publication No. US20030118610A1
; GENERAL INFORMATION:
; APPLICANT: Stern, William
; APPLICANT: Mehta, No. US20030118610A1er M.
; APPLICANT: Ray, Martha V.L.
; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE MEMBRANES
; TITLE OF INVENTION: TRANSLOCATORS
; FILE REFERENCE: P/546-247
; CURRENT APPLICATION NUMBER: US/09/997,465B
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-465B-4

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Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAVLLPVLLAAP 12

RESULT 4
US-10-116-288-1
; Sequence 1, Application US/10116288
; Publication No. US20020143142A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: 22000.0097U3
; CURRENT APPLICATION NUMBER: US/10/116,288
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/562,868

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; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(12)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288-1

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Best Local Similarity 100.0%; Pred. No. 0.03;
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Db 1 AAVLLPVLLAAP 12

RESULT 5
US-10-226-956-286
; Sequence 286, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padmini
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshi, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-226-956-286

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAVLLPVLLAAP 12

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RESULT 6
US-10-077-555-1
; Sequence 1, Application US/10077555
; Publication No. US20030077289A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Use of Cell-Penetrating Peptides to Generate Antitumor Immunity
; FILE REFERENCE: P02373US1/10200806
; CURRENT APPLICATION NUMBER: US/10/077,555
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/268,687
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-077-555-1

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
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DB 1 AAVLLPVLAAAP 12

RESULT 7
US-10-211-088-304
; Sequence 304, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 304
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Protein-derived transport peptide
US-10-211-088-304

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
|||||
DB 1 AAVLLPVLAAAP 12

RESULT 8
US-10-156-570A-27
; Sequence 27, Application US/10156570A
; Publication No. US20030125242A1
; GENERAL INFORMATION:
; APPLICANT: ROSENECKER, JOSEPH
; APPLICANT: RITTER, WOLFGANG

; APPLICANT: RUDOLPH, CARSTEN MARTIN
; APPLICANT: PLANK, CHRISTIAN
; TITLE OF INVENTION: POLYPEPTIDES COMPRISING MULTIMERS OF NUCLEAR
; TITLE OF INVENTION: LOCALIZATION SIGNALS OR OF PROTEIN TRANSDUCTION DOMAINS
; TITLE OF INVENTION: AND THEIR USE FOR TRANSFERRING NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: INTO CELLS
; FILE REFERENCE: VOS-35
; CURRENT APPLICATION NUMBER: US/10/156,570A
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: PCT/EP00/11690
; PRIOR FILING DATE: 2000-11-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: transportan
; OTHER INFORMATION: hydrophobic protein transduction domain
US-10-156-570A-27

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
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DB 1 AAVLLPVLAAAP 12

RESULT 9
US-10-126-845-1
; Sequence 1, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-10-126-845-1

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
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DB 1 AAVLLPVLAAAP 12

RESULT 10
US-10-126-845-14
; Sequence 14, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

Fri Feb 4 11:21:31 2005

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; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-10-126-845-14

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
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Db 1 AAVLLPVLLAAP 12

RESULT 11
US-10-126-845-72
; Sequence 72, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 72
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(12)
; OTHER INFORMATION: D form amino acid
US-10-126-845-72

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
   |||||
Db 1 AAVLLPVLLAAP 12

RESULT 12
US-10-136-187-1
; Sequence 1, Application US/10136187
; Publication No. US20030203865A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/136,187
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/287,786

; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-136-187-1

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
   |||||
Db 1 AAVLLPVLLAAP 12

RESULT 13
US-10-116-275-102
; Sequence 102, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20057
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 102
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Up
; OTHER INFORMATION: take Across the GIT"
US-10-116-275-102

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
   |||||
Db 1 AAVLLPVLLAAP 12

RESULT 14
US-10-144-549-19
; Sequence 19, Application US/10144549
; Publication No. US20030211590A1
; GENERAL INFORMATION:
; APPLICANT: GeneShuttle Biopharm, Inc.
; APPLICANT: Hwu, Paul L.
; TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
; FILE REFERENCE: MBHB 02-340
; CURRENT APPLICATION NUMBER: US/10/144,549
; CURRENT FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus

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; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Kaposi FGF signal sequence.
US-10-144-549-19

Query Match      100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
Db 1 AAVLLPVLAAAP 12

RESULT 15
US-10-361-208-473
; Sequence 473, Application US/10361208
; Publication No. US20040009167A1
; GENERAL INFORMATION:
; APPLICANT: Rider, Todd H.
; TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS
; FILE REFERENCE: 0050, 2041-003
; CURRENT APPLICATION NUMBER: US/10/361,208
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,359
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/355,022
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/432,386
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 473
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-361-208-473

Query Match      100.0%; Score 54; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
Db 1 AAVLLPVLAAAP 12
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Search completed: February 2, 2005, 18:56:44
Job time : 144 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2005, 18:37:38 ; Search time 38 Seconds
(without alignments)
20.943 Million cell updates/sec

Title: US-10-634-645-1

Perfect score: 54

Sequence: 1 AAVLLPVLLAAP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/6C COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/6D COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	12	3	US-09-186-170-1
2	54	100.0	12	4	US-09-562-868-1
3	54	100.0	12	4	US-09-997-4659-4
4	54	100.0	12	4	US-10-083-889-8
5	54	100.0	12	4	US-10-116-288-1
6	54	100.0	12	4	US-09-671-089-1
7	54	100.0	12	4	US-09-671-089-14
8	54	100.0	15	4	US-09-671-089-2
9	54	100.0	16	4	US-09-671-089-3
10	54	100.0	16	4	US-09-671-089-5
11	54	100.0	16	4	US-09-671-089-48
12	54	100.0	19	4	US-09-671-089-4
13	50	92.6	11	3	US-09-186-170-9
14	50	92.6	11	4	US-09-562-868-9
15	50	92.6	11	4	US-10-116-288-9
16	50	92.6	11	4	US-09-671-089-19
17	50	92.6	13	4	US-09-671-089-10
18	47	87.0	11	3	US-09-186-170-5
19	47	87.0	11	4	US-09-562-868-5
20	47	87.0	11	4	US-10-116-288-5
21	47	87.0	11	4	US-09-671-089-15
22	47	87.0	13	4	US-09-671-089-6
23	47	87.0	17	4	US-09-671-089-23
24	46	85.2	10	3	US-09-186-170-8
25	46	85.2	10	4	US-09-562-868-8
26	46	85.2	10	4	US-10-116-288-8
27	46	85.2	10	4	US-09-671-089-20

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28 46 85.2 12 4 US-09-671-089-11 Sequence 11, Appl
29 43 79.6 10 3 US-09-186-170-4 Sequence 4, Appli
30 43 79.6 10 4 US-09-562-868-4 Sequence 4, Appli
31 43 79.6 10 4 US-10-116-288-4 Sequence 4, Appli
32 43 79.6 12 4 US-09-671-089-16 Sequence 16, Appl
33 43 79.6 12 4 US-09-671-089-59 Sequence 59, Appl
34 43 79.6 14 4 US-09-671-089-7 Sequence 7, Appli
35 43 79.6 14 4 US-09-671-089-58 Sequence 58, Appli
36 43 79.6 17 4 US-09-671-089-24 Sequence 24, Appli
37 42 77.8 9 3 US-09-186-170-7 Sequence 7, Appli
38 42 77.8 9 4 US-09-562-868-7 Sequence 7, Appli
39 42 77.8 9 4 US-10-116-288-7 Sequence 7, Appli
40 42 77.8 9 4 US-09-671-089-21 Sequence 21, Appl
41 42 77.8 11 4 US-09-671-089-12 Sequence 12, Appl
42 40 74.1 1246 4 US-09-919-497-85 Sequence 85, Appl
43 40 74.1 1247 4 US-09-961-403-14 Sequence 14, Appl
44 39 72.2 9 3 US-09-186-170-3 Sequence 3, Appli
45 39 72.2 9 4 US-09-562-868-3 Sequence 3, Appli

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ALIGNMENTS

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RESULT 1
US-09-186-170-1
; Sequence 1, Application US/09186170
; Patent No. 6248558
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6248558
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: VU9841
; CURRENT APPLICATION NUMBER: US/09/186,170
; CURRENT FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/080,083
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(12)
; PUBLICATION INFORMATION:
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
; RELEVANT RESIDUES: 1 TO 12
US-09-186-170-1

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Query Match 100.0%; Score 54; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAVLLPVLLAAP 12
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DB 1 AAVLLPVLLAAP 12

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Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 4
US-10-083-889-8
; Sequence 8, Application US/10083889
; Patent No. 6673894
; GENERAL INFORMATION:
; APPLICANT: Zahner, Joseph E.
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
; FILE REFERENCE: 16850-7331
; CURRENT APPLICATION NUMBER: US/10/083,889
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/271,798
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mammalian
US-10-083-889-8

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 5
US-10-116-288-1
; Sequence 1, Application US/10116288
; Patent No. 6780843
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6780843
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: 22000.009703
; CURRENT APPLICATION NUMBER: US/10/116,288
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/562,868
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(12)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.

US-09-562-868-1
; Sequence 1, Application US/09562868
; Patent No. 6432680
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6432680
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: 22000.009702
; CURRENT APPLICATION NUMBER: US/09/562,868
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(12)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-09-562-868-1

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVLLPVLLAAP 12
Db 1 AAVLLPVLLAAP 12

RESULT 3
US-09-997-465B-4
; Sequence 4, Application US/09997465B
; Patent No. 6673574
; GENERAL INFORMATION:
; APPLICANT: Stern, William
; APPLICANT: Mehta, No. 6673574er M.
; APPLICANT: Ray, Martha V.L.
; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE MEMBRAN
; TITLE OF INVENTION: TRANSLOCATORS
; FILE REFERENCE: P/546-247
; CURRENT APPLICATION NUMBER: US/09/997,465B
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-997-465B-4

Query Match 100.0%; Score 54; DB 4; Length 12;
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; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: "Permeabilizing""
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288-1

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Query Match	100.0%	Score 54;	DB 4;	Length 12;
Best Local Similarity	100.0%;	Pred. No. 0.0063;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 AAVLLPVLLAAP 12
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Db 1 AAVLLPVLLAAP 12

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RESULT 6
US-09-671-089-1
; Sequence 1, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-1

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Query Match	100.0%	Score 54;	DB 4;	Length 12;
Best Local Similarity	100.0%	Pred. No. 0.0063;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 AAVLLPVLLAAP 12
|||
Db 1 AAVLLPVLLAAP 12

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RESULT 7
US-09-671-089-14
; Sequence 14, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-14

```

Query Match 100.0%; Score 54; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels

Qy 1 AAVLLPVLLAAP 12
| | | | | | | | | |
Db 1 AAVLLPVLLAAP 12

```

RESULT 8
US-09-671-089-2
; Sequence 2, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Inelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)..(15)
; OTHER INFORMATION: linked to FITC-LC
US-09-671-089-2

```

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Query Match      100.0%; Score 54; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Caps 0;
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Qy 1 AAVLLPVLLAAP 12
|||
Db 4 AAVLLPVLLAAP 15

```

RESULT 9
US-09-671-089-3
; Sequence 3, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-3

```

```
Query Match      100.0%; Score 54; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 AAVLLPVLLAAP 12

Fri Feb 4 11:21:31 2005

Db 5 AAVLLPVLLAAP 16
|||||

RESULT 10
US-09-671-089-5
; Sequence 5, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide, cyclic
US-09-671-089-5

Query Match 100.0%; Score 54; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
|||||
Db 4 AAVLLPVLLAAP 15

RESULT 11
US-09-671-089-48
; Sequence 48, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671.089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dansylated membrane translocating peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: dansylated
US-09-671-089-48

Query Match 100.0%; Score 54; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
|||||
Db 5 AAVLLPVLLAAP 16

RESULT 12

US-09-671-089-4
; Sequence 4, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671.089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-4

Query Match 100.0%; Score 54; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
|||||
Db 4 AAVLLPVLLAAP 15

RESULT 13
US-09-186-170-9
; Sequence 9, Application US/09186170
; Patent No. 6248558
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 6248558
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: VU9841
; CURRENT APPLICATION NUMBER: US/09/186,170
; CURRENT FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(11)
; PUBLICATION INFORMATION:
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
; RELEVANT RESIDUES: 1 TO 12
US-09-186-170-9

Query Match 92.6%; Score 50; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 AVLLPVLLAAP 12
|||||
DB 1 AVLLPVLLAAP 11

RESULT 14

US-09-562-868-9
; Sequence 9, Application US/09562868
; Patent No. 6432680
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Proteins with Cell Membrane Translocating Activity"
; Patent No. 6432680
; FILE REFERENCE: 22000.009702
; CURRENT APPLICATION NUMBER: US/09/562,868
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(11)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-09-562-868-9

Query Match 92.6%; Score 50; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 AVLLPVLLAAP 12
|||||
DB 1 AVLLPVLLAAP 11

US-10-116-288-9
; Sequence 9, Application US/10116288
; Patent No. 6780843
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Proteins with Cell Membrane Translocating Activity"
; Patent No. 6780843
; FILE REFERENCE: 22000.009703
; CURRENT APPLICATION NUMBER: US/10/116,288

Query Match 92.6%; Score 50; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 AVLLPVLLAAP 12
|||||
DB 1 AVLLPVLLAAP 11

RESULT 15

US-10-116-288-9
; Sequence 9, Application US/10116288
; Patent No. 6780843
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Proteins with Cell Membrane Translocating Activity"
; Patent No. 6780843
; FILE REFERENCE: 22000.009703
; CURRENT APPLICATION NUMBER: US/10/116,288

US-10-116-288-9
; Sequence 9, Application US/10116288
; Patent No. 6780843
; GENERAL INFORMATION:
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Donahue, John P.
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Proteins with Cell Membrane Translocating Activity"
; Patent No. 6780843
; FILE REFERENCE: 22000.009703
; CURRENT APPLICATION NUMBER: US/10/116,288
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: 09/186,170
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/080,083
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of peptide which transports proteins
; OTHER INFORMATION: through the cell membrane into the cell.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(11)
; PUBLICATION INFORMATION:
; AUTHORS: Rojas, M. et al.
; TITLE: "Genetic Engineering of Proteins with Cell Membrane
; TITLE: Permeability"
; JOURNAL: Nature Biotechnology
; VOLUME: 16
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288-9

Query Match 92.6%; Score 50; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 AVLLPVLLAAP 12
|||||
DB 1 AVLLPVLLAAP 11

Search completed: February 2, 2005, 18:45:41
Job time : 39 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2005, 18:35:13 ; Search time 45 Seconds
(without alignments)
25.658 Million cell updates/sec

Title: US-10-634-645-1

Perfect score: 54

Sequence: 1 AAVLLPVLLAAP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	74.1	390	2 A72698	hypothetical prote
2	40	74.1	1247	1 MMHUND	nidogen precursor
3	39	72.2	303	2 B83336	hypothetical prote
4	39	72.2	493	2 AB3032	hypothetical prote
5	39	72.2	602	2 A96254	exsE protein (AJ22
6	38	70.4	175	2 B44102	di-N-acetylchitobi
7	38	70.4	249	2 T35589	probable secreted
8	38	70.4	297	2 AF3275	transporter, dme f
9	38	70.4	398	2 C82614	riboflavin biosynt
10	37	68.5	370	2 D86957	probable inosine-5
11	37	68.5	375	1 S72812	IMP dehydrogenase-
12	37	68.5	389	2 H82825	transport protein
13	37	68.5	409	2 C75511	alanyl-tRNA synth
14	37	68.5	420	2 T05877	hypothetical prote
15	37	68.5	788	2 C95046	helicase, probable
16	37	68.5	788	2 C97917	exonuclease V [imp
17	36	66.7	158	2 A12821	conserved hypothet
18	36	66.7	163	2 A97600	hypothetical prote
19	36	66.7	208	2 E97899	hypothetical prote
20	36	66.7	235	2 T19408	hypothetical prote
21	36	66.7	241	2 T05040	nodulin-26-like pr
22	36	66.7	259	2 A98098	hypothetical prote
23	36	66.7	259	2 E85943	hypothetical prote
24	36	66.7	259	2 H65071	hypothetical prote
25	36	66.7	308	2 H85214	nodulin-26-like pr
26	36	66.7	354	2 AC0389	phosphate binding
27	36	66.7	387	2 T02780	probable conjugal
28	36	66.7	411	2 H75376	hypothetical prote
29	36	66.7	582	2 I49673	matrix metalloprot

ALIGNMENTS

RESULT 1

A72698

hypothetical protein APE1001 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: A72698

Rikawabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: A72698

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-390 <KAW>

A:Cross-references: UNIPROT:Q9YDB2; DDBJ:AP000060; NID:G5104188; PIDN:BAA79985.1; PID:dl

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1001

Query Match 74.1%; Score 40; DB 2; Length 390;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12
|||:|:|:
DB 180 AAKLLPLLAAP 191

RESULT 2

MMHUND

nidogen precursor - human

N:Alternate names: entactin

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: A33322; A32437; A61367

R:Nagayoshi, T.; Sanborn, D.; Hickok, N.J.; Olsen, D.R.; Fazio, M.J.; Chu, M.L.; Knowl

DNA 8, 581-594, 1989

A>Title: Human nidogen: complete amino acid sequence and structural domains deduced from

A:Reference number: A33322; MUID:90091745; PMID:2574658

A:Accession: A33322

A:Molecule type: mRNA

A:Residues: 1-1247 <NAG>

A:Cross-references: UNIPROT:P14543; EMBL:M30269

R:Olsen, D.R.; Nagayoshi, T.; Fazio, M.; Mattei, M.G.; Passage, E.; Weil, D.; Timpl, R.;

Am. J. Hum. Genet. 44, 876-885, 1989

A>Title: Human nidogen: cDNA cloning, cellular expression, and mapping of the gene to chr

A:Reference number: A32437; MUID:89270475; PMID:2471408

A:Accession: A32437

A:Molecule type: mRNA

A:Residues: 667-1247 <OLS>

A:Cross-references: EMBL:M27445; NID:G602466; PIDN:AAA57261.1; PID:G602467

30	66.7	582	2	I38028
31	66.7	582	2	I84471
32	66.7	615	2	AH2248
33	66.7	623	2	T35377
34	66.7	1706	2	T39305
35	64.8	94	2	T23251
36	64.8	136	2	I49013
37	64.8	138	2	G73778
38	64.8	147	2	H82172
39	64.8	202	2	I46688
40	64.8	246	2	T25330
41	64.8	252	2	H72469
42	64.8	351	2	T08015
43	64.8	359	2	JC7280
44	64.8	376	2	T30277
45	64.8	388	1	S22387

matrix metalloprot
matrix metalloprot
protease [import
proteasome membra
proteinkinase - f
hypothetical prote
thymic shared anti
hypothetical prote
heat shock protein
complement compone
hypothetical prote
hypothetical prote
probable malate de
cytokine receptor-
hypothetical prote
cuticle-degrading

A>Note: the authors translated the codon AAG for residue 966 as Cys
R;Pazio, M.J.; O'Leary, J.; Kaeheari, V.M.; Chen, Y.Q.; Saitta, B.; Uitto, J.
J. Invest. Dermatol. 97, 281-285, 1991
A>Title: Human nidogen gene: structural and functional characterization of the 5'-flanki
A;Reference number: A61367; MUID:91302882; PMID:1906509
A;Accession: A61367
A;Molecule type: DNA
A;Residues: 1-28 <PAZ>
C;Comment: This protein is a basement membrane glycoprotein that forms a complex with la
C;Genetics:
A;Gene: GDB:NID
A;Cross-references: GDB:120236; OMIM:131390
A;Map position: 1q43-1q43
C;Superfamily: nidogen; EGF homology; LDL receptor YWTD-containing repeat homology; thy
C;Keywords: basement membrane; beta-hydroxyasparagine; calcium binding; cell binding; co
protein
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1247/Product: nidogen #status predicted <MAT>
F;390-425/Domain: EGF homology <EG1>
F;672-708/Domain: EGF homology <EG2>
F;702-704/Region: cell attachment (R-G-D) motif
F;714-750/Domain: EGF homology <EG3>
F;762-800/Domain: EGF homology <EG4>
F;806-839/Domain: EGF homology <EG5>
F;849-919/Domain: thyroglobulin type I repeat homology <THY1>
F;990-1032/Domain: LDL receptor YWTD-containing repeat homology <YW1>
F;1033-1075/Domain: LDL receptor YWTD-containing repeat homology <YW2>
F;1076-1120/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;1121-1160/Domain: LDL receptor YWTD-containing repeat homology <YW4>
F;1161-1197/Domain: LDL receptor YWTD-containing repeat homology <YW5>
F;1212-1243/Domain: EGF homology <EG6>
F;1289,296/Binding site: sulfate (Tyr) (covalent) #status predicted
F;729,819/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;756/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of laminin) #status predi
F;1137/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.1%; Score 40; DB 1; Length 1247;
Best Local Similarity 72.7%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVLLPVLAAAP 12
|:|:|:|:|:|
DB 15 ALLLPVLAAAP 25

RESULT 3
B83336
hypothetical protein PA2474 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83336
B;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83336
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <STO>
A;Cross-references: UNIPROT:Q91108; GB:AE004675; GB:AE004091; NID:g9948522; PIDN:AA05086
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2474

Query Match 72.2%; Score 39; DB 2; Length 303;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAALLPVLAAAP 12
|:|:|:|:|:|
DB 96 AALLPVLAAAP 107

A:Title: Cloning and expression of the cDNA sequence encoding the lysosomal glycosidase
 A:Reference number: A44102; MUID:92406917; PMID:1527079
 A:Accession: B44102

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-175 <FIS>

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIP:113986)

C:Keywords: glycosidase; hydrolase

Query Match 70.4%; Score 38; DB 2; Length 175;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12

DB 23 APFLLPVLLALP 34

RESULT 7

T35589 probable secreted protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C:Accession: T35589; S37564

R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z1583

A:Accession: T35589

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-249 <SAU>

A:Cross-references: UNIPROT:P40179; EMBL:AL031317; PIDN:CAA20416.1; GSPDB:GN00070; SCOE

A:Experimental source: strain A3(2)

R:Kuchene, A.M.; Kleser, K.; Hopwood, D.; Thompson, C.; Mazodier, P.

submitted to the EMBL Data Library, September 1993

A:Description: Molecular characterization of two groEL genes in Streptomyces coelicolor

A:Reference number: S37564

A:Accession: S37564

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 121-249 <DUC>

A:Cross-references: EMBL:X75206; NID:g406595; PIDN:CAA53017.1; PID:g406596

C:Genetics:

A:Gene: SCOE:SC6G4.38

Query Match 70.4%; Score 38; DB 2; Length 249;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLLAAP 12

DB 14 AALLPVLALLP 25

RESULT 8

AF3275

A:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: AF3275

R:DelVecchio, V.G.; Kaprat, R.J.; Patra, G.; Muir, C.; Loeb, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: AF3275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <KUR>

A:Cross-references: UNIPROT:Q8YJ99; GB:AE008917; PIDN:AAL51369.1; PID:g17982069; GSPDB:G

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI0187

A:Map position: 1

Query Match 70.4%; Score 38; DB 2; Length 297;

Best Local Similarity 80.0%; Pred. No. 35;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVLLPVLLA 10

DB 161 AALLPVLLA 170

RESULT 9

C82614

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: C82614

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: For a complete list of authors see reference number A59328 below

A:Accession: C82614

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-398 <SIM>

A:Cross-references: UNIPROT:Q9PBZ3; GB:AE004018; GB:AE003849; NID:g9107093; PIDN:AAF84794

A:Experimental source: strain 945c

R:Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuran, E.E.; Laigre

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki

A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

C:Contents: annotation

C:Genetics:

A:Gene: XF1992

C:Superfamily: Azospirillum cyclohydrolase II; cyclohydrolase homology

Query Match 70.4%; Score 38; DB 2; Length 398;
 Best Local Similarity 63.6%; Pred. No. 46;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVLLPVLLAAP 12

DB 131 ALLPVAIVAAP 141

RESULT 10

D86957

probable inosine-5'-monophosphate dehydrogenase [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: D86957

R:Coile, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; -Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: D86957

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-370 <STO>

Fri Feb 4 11:21:32 2005

A;Cross-references: GB:AL450380; NID:gl3092663; PIDN:CAC29896.1; GSPDB:GN00147

C;Genetics:

A;Gene: guaB3

C;Superfamily: Synechocystis IMP dehydrogenase homolog; IMP dehydrogenase amino-terminal

Query Match 68.5%; Score 37; DB 2; Length 370;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLAA 11
||| |||||
DB 141 AAVLLPVLAA 151

RESULT 11

IMP dehydrogenase-related protein guaB1 - Mycobacterium leprae

N;Alternate names: B1620 C2 193 protein

C;Species: Mycobacterium leprae

C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 09-Jul-2004

C;Accession: S72812

R;Smith, D.R.; Robinson, K.

submitted to the EMBL Data Library, November 1993

A;Description: Mycobacterium leprae cosmid B1620.

A;Reference number: S72584

A;Accession: S72812

A;Molecule type: DNA

A;Residues: 1-375 <SMI>

A;Cross-references: UNIPROT:Q49721; EMBL:U00015; NID:g466931; PIDN:AAC43221.1; PID:g4669

C;Comment: This sequence is similar to IMP dehydrogenase at the amino end and at the car

name and GMP reductase.

C;Genetics:

A;Gene: guaB1

C;Superfamily: Synechocystis IMP dehydrogenase homolog; IMP dehydrogenase amino-terminal

F;14-79/Domain: IMP dehydrogenase amino-terminal homology <IDHN>

F;127-363/Domain: IMP dehydrogenase catalytic homology <IDHC>

Query Match 68.5%; Score 37; DB 1; Length 375;

Best Local Similarity 81.8%; Pred. No. 65;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVLLPVLAA 11
||| |||||
DB 146 AAVLLPVLAA 156

RESULT 12

H82825

transport protein XF0281 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: H82825

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: H82825

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-389 <SIM>

A;Cross-references: UNIPROT:Q9PGL7; GB:AE003881; GB:AE003849; NID:g9105093; PIDN:AAF8309

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0281

Query Match 68.5%; Score 37; DB 2; Length 389;

Best Local Similarity 88.9%; Pred. No. 67;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAVLLPVLAA 10
||| |||||
DB 69 AAVLLPVLAA 77

RESULT 13

C75511

alanyl-tRNA synthetase-related protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: C75511

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: C75511

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-409 <WHI>

A;Cross-references: UNIPROT:Q9RX13; GB:AE001909; GB:AE000513; NID:g6458188; PIDN:AAF1008

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0502

A;Map position: 1

Query Match 68.5%; Score 37; DB 2; Length 409;

Best Local Similarity 66.7%; Pred. No. 70;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
||| |||||
DB 333 AAVLLPVLTAAP 344

RESULT 14

T05877

hypothetical protein T29A15.210 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05877

R;Bavan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Hol

submitted to the Protein Sequence Database, March 1999

A;Reference number: Z15455

A;Accession: T05877

A;Molecule type: DNA

A;Residues: 1-420 <BEV>

A;Cross-references: UNIPROT:Q9T094; EMBL:AL035602

A;Experimental source: cultivar Columbia; BAC clone T29A15

C;Genetics:

A;Map position: 4

A;Introns: 51/1; 99/2; 155/3; 246/1; 334/3; 378/3

A;Note: T29A15.210

C;Superfamily: Arabidopsis thaliana hypothetical protein F2K15.170

Query Match 68.5%; Score 37; DB 2; Length 420;

Best Local Similarity 63.6%; Pred. No. 72;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVLLPVLAA 11
||| |||||

Db 325 AALLPILMTA 335

RESULT 15

C95046
 helicasase, probable (imported) - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: C95046
 R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; PMID:21357209; PMID:11463916
 A:Accession: C95046
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-788 <KUR>
 A:Cross-references: UNIPROT:Q97SG8; GB:AE005672; PIDN:AAK74564.1; PID:G14971869; GSPDB:C
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP0401

Query Match 68.5%; Score 37; DB 2; Length 788;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVLLAAP 12
 ||:||||
 Db 384 LPVLLAAP 391

Search completed: February 2, 2005, 18:45:02
 Job time : 51 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2005, 18:27:02 ; Search time 194 Seconds
(without alignments)
35.590 Million cell updates/sec

Title: US-10-634-645-1

Perfect score: 54

Sequence: 1 AAVLLPVLAAAP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	79.6	340	2 Q8FRS4	Q8frs4 corynebacte
2	42	77.8	291	2 Q98FS7	Q98fs7 rhizobium 1
3	41	75.9	356	2 Q8H8C7	Q8h8c7 oryza sativ
4	40	74.1	133	2 Q6ND81	Q6nd81 rhodospheuo
5	40	74.1	133	2 CAE25672	CAe25672 rhodopseu
6	40	74.1	195	2 Q7PS92	Q7ps92 anophelies g
7	40	74.1	195	2 Q9BIH2	Q9bih2 anophelies g
8	40	74.1	279	2 Q89D56	Q89d56 bradyrhizob
9	40	74.1	390	2 Q9YDB2	Q9ydb2 aeropyrum p
10	40	74.1	497	2 Q6N2W2	Q6n2w2 rhodopseuo
11	40	74.1	497	2 CAE29377	CAe29377 rhodopseu
12	40	74.1	639	2 Q9K4H5	Q9k4h5 streptomyce
13	40	74.1	659	2 Q82NQ4	Q82nq4 streptomyce
14	40	74.1	831	2 Q89RR5	Q89rr5 bradyrhizob
15	40	74.1	1114	2 Q86XD7	Q86xd7 homo sapien
16	40	74.1	1247	1 NIDO_HUMAN	P14543 homo sapien
17	39	72.2	43	1 PSBY_SYNBL	Q8dkm3 synchococc
18	39	72.2	253	2 Q73HU0	Q73hu0 wolbachia p
19	39	72.2	253	2 AAS14173	Aas14173 wolbachia
20	39	72.2	303	2 Q91108	Q91108 pseudomonas
21	39	72.2	481	2 Q95W90	Q95w90 trypanosoma
22	39	72.2	493	2 Q8U966	Q8u966 agrobacteri
23	39	72.2	498	2 Q7VU08	Q7vu08 bordetella
24	39	72.2	582	2 Q99PG1	Q99pg1 cricetus
25	39	72.2	602	2 Q7CTH2	Q7cth2 agrobacteri
26	39	72.2	628	2 Q89IJ7	Q89ij7 bradyrhizob
27	39	72.2	3970	2 Q93HI8	Q93hi8 streptomyce
28	38	70.4	38	1 PSBY_PROMM	P59909 prochloroco
29	38	70.4	111	2 Q9NE12	Q9nei2 leishmania
30	38	70.4	131	2 Q8KP20	Q8kzp0 thermus the
31	38	70.4	131	2 Q72JCO	Q72jco thermus the

RESULT 1

Q8FRS4 PRELIMINARY; PRT; 340 AA.
AC Q8FRS4;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Putative iron transport membrane protein.
GN OrderedLocusNames=CE0685;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579(2003).
DR EMBL: AP005216; BAC17495.1; -.
DR HSSP: P06609; 1LVV.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000522; FecD.
DR Pfam: PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 340 AA; 34818 MW; 14B047C6A943A576 CRC64;

Query Match 79.6%; Score 43; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVLLPVLAA 11
| | | | | | | | | |
DB 211 AVLLPVLAA 220

RESULT 2

Q98FS7 PRELIMINARY; PRT; 291 AA.
AC Q98FS7;
DT 01-OCT-2001 (TremBLrel. 18, Created)
DT 01-OCT-2001 (TremBLrel. 18, Last sequence update)
DE 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE M13636 protein.
OS OrderedLocusNames=mlr3636;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Aas81202 thermus t
Q01458 bos taurus
Q62334 oryza sativ
Bad16090 oryza sat
Q6cpr9 kluyveromyc
Q8kvc4 ralatonia s
Q7eyb9 oryza sativ
Bad01437 oryza sat
Bac99441
P40179 streptomyce
Q89tk8 bradyrhizob
Q8fyj9 brucella su
Q8y199 brucella me
Q755p8 ashbya goss

```

OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NAFF303099;
RX MEDLINE=21082936; PubMed=11214974;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti (supplement)." ;
RL DNA Res. 7:381-406(2000).
DR ENBL: AP003002; BAB50490.1; -.
KW Complete proteome.
SQ SEQUENCE 291 AA; 31162 MW; 3C6B651E33A79EE2 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 291;
Best Local Similarity 58.3%; Pred. No. 45;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
DB 115 SAIFLPVLIAP 126
:::|||||
115 SAIFLPVLIAP 126

RESULT 3
Q8H8C7 Q8H8C7 PRELIMINARY; PRT; 356 AA.
ID Q8H8C7
AC Q8H8C7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein OJ1006F06.19.
GN Name=OJ1006F06.19;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
RA Currie J., Collura K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL: AC099399; AAN05509.1; -.
DR Gramineae; Q8H8C7; -.
DR GO: GO:0016998; P:cell wall catabolism; IEA.
DR InterPro: IPR002482; LysM.
DR Pfam: PF01476; LysM; 2.
DR SMART: SM00257; LysM; 2.
KW Hypothetical protein.
SQ SEQUENCE 356 AA; 37200 MW; 007D7BED10AB98FE CRC64;

Query Match 75.9%; Score 41; DB 2; Length 356;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
DB 115 SAIFLPVLIAP 126
:::|||||
115 SAIFLPVLIAP 126

RESULT 4
Q6ND81 Q6ND81 PRELIMINARY; PRT; 133 AA.
ID Q6ND81
AC Q6ND81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocustNames=RPA0228;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris." ;
RL Nat. Biotechnol. 22:55-61(2004).
DR ENBL: BX572593; CAE25672.1; -.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 37
SQ SEQUENCE 133 AA; 14481 MW; E22F622199718B5B CRC64;

Query Match 74.1%; Score 40; DB 2; Length 133;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVLLPVLAA 11
DB 15 AAVLLPVLAA 25
|||||
15 AAVLLPVLAA 25

RESULT 5
CAE25672 CAE25672 PRELIMINARY; PRT; 133 AA.
ID CAE25672
AC CAE25672;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor.
GN RPA0228.
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris." ;
RL Nat. Biotechnol. 22:55-61(2004).
DR ENBL: BX572593; CAE25672.1; -.
KW Hypothetical protein; Signal.
FT SIGNAL 1 37
SQ SEQUENCE 133 AA; 14481 MW; E22F622199718B5B CRC64;

Query Match 74.1%; Score 40; DB 2; Length 133;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVLLPVLAAAP 12
DB 15 AAVLLPVLAAAP 25
|||||
15 AAVLLPVLAAAP 25

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QY 1 AAVLLPVLAA 11
 DB 15 AAVLLPVLAA 25
 RESULT 6
 Q7PS92 PRELIMINARY; PRT; 195 AA.
 AC Q7PS92;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE ENSANGP0000018919.
 GN Name=ENSANG0000016430;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008844; EAA05987.2; -.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR PROSITE; P500141; ASP_PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 195 AA; 20951 MW; 3DF52FD0418AF6A7 CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 195;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAAAP 12
 DB 14 AAVLLQPLLAAP 25
 RESULT 7
 Q9BIH2 PRELIMINARY; PRT; 195 AA.
 AC Q9BIH2;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein gSG10 precursor.
 GN Name=gSG10;
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GSUA;
 RX MEDLINE=22057806; PubMed=12062411;
 RA Lanfrancotti A., Lombardo F., Santolamazza F., Veneri M.,
 RA Castriagnano T., Coluzzi M., Arca' B.;
 RT "Novel cDNAs encoding salivary proteins from the malaria vector
 RT Anopheles gambiae.";
 RL FEBS Lett. 517:67-71 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GSUA;
 RA Arca B.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ302660; CAC3525.1; -.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR PROSITE; P500141; ASP_PROTEASE; UNKNOWN_1.
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 35 Potential.

SQ SEQUENCE 195 AA; 20951 MW; 3DF52FD0418AF6A7 CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 195;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAAAP 12
 DB 14 AAVLLQPLLAAP 25
 RESULT 8
 Q89D56 PRELIMINARY; PRT; 279 AA.
 ID Q89D56;
 AC Q89D56;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE B1r7587 protein.
 GN OrderedLocusNames=b1r7587;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197 (2002).
 DR EMBL; AP005962; BAC52852.1; -.
 KW Complete proteome.
 SQ SEQUENCE 279 AA; 29666 MW; 27651945C0E13C39 CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 279;
 Best Local Similarity 58.3%; Pred. No. 98;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAAAP 12
 DB 115 AAVLLPVIQTP 126
 RESULT 9
 Q9YDB2 PRELIMINARY; PRT; 390 AA.
 ID Q9YDB2;
 AC Q9YDB2;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Hypothetical protein APE1001.
 GN OrderedLocusNames=APE1001;
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jinno K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyana A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";

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RA DNA Res. 6:83-101(1999).
 RT EMBL; AF000060; BAA79985.1; --
 RL PIR; A72698; A72698.
 DR Complete proteome; Hypothetical protein.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 390 AA; 41090 MW; 9E9D66EEAEFD207 CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 390;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAAAP 12
 ||:||||:
 Qb 180 AAKLLPVLAAAP 191
 ||:||||:
 RESULT 10
 Q6N2W2 PRELIMINARY; PRT; 497 AA.
 AC Q6N2W2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein precursor.
 GN OrderedLocustNames=RPA3936;
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
 Harrison F.H., Gibson J., Harwood C.S.;
 RA "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris."
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572605; CAE29377.1; --
 KW Complete proteome; Hypothetical protein; Signal.
 FT SIGNAL 1 30 Potential.
 SQ SEQUENCE 497 AA; 54125 MW; 6A764989856F441E CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 497;
 Best Local Similarity 72.7%; Pred. No. 1.7e+02;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAA 11
 ||:||||:
 Qb 20 AAVLLPVLAA 30
 ||:||||:
 RESULT 11
 CAE29377 PRELIMINARY; PRT; 497 AA.
 AC CAE29377;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein precursor.
 GN RPA3936.
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L.,
 Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
 Harrison F.H., Gibson J., Harwood C.S.;
 RA "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris."
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572605; CAE29377.1; --
 KW Complete proteome; Hypothetical protein; Signal.
 FT SIGNAL 1 30 Potential.
 SQ SEQUENCE 497 AA; 54125 MW; 6A764989856F441E CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 497;
 Best Local Similarity 72.7%; Pred. No. 1.7e+02;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAA 11
 ||:||||:
 Qb 20 AAVLLPVLAA 30
 ||:||||:
 RESULT 12
 Q9K4H5 PRELIMINARY; PRT; 639 AA.
 AC Q9K4H5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein SCO7250.
 GN OrderedLocustNames=SCO7250; ORFNAMES=SC7A12.17c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 Hopwood D.A.;
 RA "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL; AL939130; CAB94064.1; --
 DR GO; GO:0008745; F:N-acetylglucosyl-L-alanine amidase activity; IEA.
 DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
 DR InterPro; IPR002502; Amidase 2.
 DR Pfam; PF01510; Amidase 2; 1.
 DR SMART; SM00644; Ami 2; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 639 AA; 68049 MW; 86A67634CFE1C3EC CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 639;
 Best Local Similarity 75.0%; Pred. No. 2.1e+02;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAAAP 12
 ||:||||:
 Qb 7 AALLPVLGAAP 18
 ||:||||:
 RESULT 13
 Q82NQ4 PRELIMINARY; PRT; 659 AA.
 ID Q82NQ4
 AC Q82NQ4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative secreted amidase.

RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RL photosynthetic bacterium Rhodopseudomonas palustris."
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572605; CAE29377.1; --
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 30 Potential.
 SQ SEQUENCE 497 AA; 54125 MW; 6A764989856F441E CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 497;
 Best Local Similarity 72.7%; Pred. No. 1.7e+02;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAA 11
 ||:||||:
 Qb 20 AAVLLPVLAA 30
 ||:||||:
 RESULT 12
 Q9K4H5 PRELIMINARY; PRT; 639 AA.
 AC Q9K4H5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein SCO7250.
 GN OrderedLocustNames=SCO7250; ORFNAMES=SC7A12.17c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 Hopwood D.A.;
 RA "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL; AL939130; CAB94064.1; --
 DR GO; GO:0008745; F:N-acetylglucosyl-L-alanine amidase activity; IEA.
 DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
 DR InterPro; IPR002502; Amidase 2.
 DR Pfam; PF01510; Amidase 2; 1.
 DR SMART; SM00644; Ami 2; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 639 AA; 68049 MW; 86A67634CFE1C3EC CRC64;
 Query Match 74.1%; Score 40; DB 2; Length 639;
 Best Local Similarity 75.0%; Pred. No. 2.1e+02;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAVLLPVLAAAP 12
 ||:||||:
 Qb 7 AALLPVLGAAP 18
 ||:||||:
 RESULT 13
 Q82NQ4 PRELIMINARY; PRT; 659 AA.
 ID Q82NQ4
 AC Q82NQ4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative secreted amidase.

GO	GO:0016301	F-kinase activity; IEA.
GO	GO:0016740	F-transferase activity; IEA.
GO	GO:0000156	F-two-component response regulator activity; IEA.
GO	GO:0000155	F-two-component sensor molecule activity; IEA.
GO	GO:0007600	P-sensory perception; IEA.
GO	GO:0000160	P-two-component signal transduction system (p. . ; IEA.
DR	InterPro: IPR003594	ATPbind ATPase.
DR	InterPro: IPR004358	Bact_sens_pr_C.
DR	InterPro: IPR011006	Chey_kinase.
DR	InterPro: IPR005467	His_kinase.
DR	InterPro: IPR003661	His_kinA_N.
DR	InterPro: IPR009082	His_kin_homodim.
DR	InterPro: IPR001789	Response_reg.
DR	Pfam: PF02518	HATPase_c; 1.
DR	Pfam: PF00512	Hiska; 1.
DR	Pfam: PF00072	Response_reg; 1.
DR	PRINTS: PR00344	BCTRLSENSOR.
DR	SMART: SM00387	HATPase_c; 1.
DR	SMART: SM00388	Hiska; 1.
DR	SMART: SM00448	REC; 1.
DR	PROSITE: PS01109	HIS_KIN; 1.
DR	PROSITE: PS01110	RESPONSE_REGULATORY; 1.
KW	Complete proteome; Kinase; Phosphorylation; Sensory transduction; Transference.	
QY	SEQUENCE 831 AA; 89854 MW; F15F92E7446541E0 CRC64;	
DB	Query Match 74.1%; Score 40; DB 2; Length 831;	
	Best Local Similarity 66.7%; Pred. No. 2,7e+02;	
	Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
QY	1 AAVLLPVLLAAP 12	
DB	768 AAPALPILAAP 779	
RESULT 15		
Q86XD7	PRELIMINARY; PRT; 1114 AA.	
AC	Q86XD7	
ID	Q86XD7	
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	NID protein.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxId=9606;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Testis;	
RC	MEDLINE=22388257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udwin T.B., Teshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley A.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez R.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	
RT	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RP	[2]	
RP	SEQUENCE FROM N.A.	

RC TISSUE-Testis;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC045606; AAH45606.1; -.
DR HSSP; P10493; 1GL4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR011044; Amine_DH_B_like.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006605; G2F.
DR InterPro; IPR009017; GFP like.
DR InterPro; IPR06210; IEGF.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR InterPro; IPR010362; NIDO.
DR InterPro; IPR003886; Nidogen ext.
DR InterPro; IPR000716; Thyroglobulin_1.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF07474; G2F; 1.
DR Pfam; PF00058; Ldl_recept_b; 3.
DR Pfam; PF06119; NIDO; 1.
DR Pfam; PF00086; Thyroglobulin_1; 1.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00682; G2F; 1.
DR SMART; SM0135; LY; 5.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00211; TY; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS00026; EGF 3; 1.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
KW EGF-like domain.
SQ SEQUENCE 1114 AA; 12209 MW; 854FC97ADFCC75D2 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 1114;
Best Local Similarity 72.7%; Pred. No. 3.5e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 AVILPVLLAP 12
Db 15 ALLPLLLAGP 25

Search completed: February 2, 2005, 18:44:09
Job time: 198 secs